

AX425084
 LOCUS 121 bp DNA linear PAT 07 JAN 2002
 DEFINITION Sequence 1221 from Patent WO/992512.
 ACCESSION AX425084
 VERSION AX425084.1 GI:18095848
 KEYWORDS tomato.
 SOURCE Lycopersicon esculentum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
 REFERENCE 1
 AUTHORS Kniep, E.B., Gampel, H.B., Rice, M.C., and Kim, J.
 TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
 JOURNAL Patent: WO 0192512-A 1221 06-DEC-2001;
 UNIVERSITY OF DELAWARE (US)
 FEATURES
 source
 1..121
 /organism="Lycopersicon esculentum"
 /db_xref="taxon:4081"
 BASE COUNT 43 a 21 c 26 g 43 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 20.7 Length: 121
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-856-070-26 (1-c) x AX425084 (1-121)
 QY 1 GluAspTyrGluGlu 5
 |||||
 DB 66 CAACACTATGAGAA 52
 RESULT 2
 LOCUS AX425084 121 bp DNA linear PAT 07 JAN 2002
 DEFINITION Sequence 1222 from Patent WO/992512.
 ACCESSION AX425084
 VERSION AX425084.1 GI:18095849
 KEYWORDS tomato.
 SOURCE Lycopersicon esculentum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
 REFERENCE 1
 AUTHORS Kniep, E.B., Gampel, H.B., Rice, M.C., and Kim, J.
 TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
 JOURNAL Patent: WO 0192512-A 1222 06-DEC-2001;
 UNIVERSITY OF DELAWARE (US)
 FEATURES
 source
 1..121
 /organism="Lycopersicon esculentum"
 /db_xref="taxon:4081"
 BASE COUNT 43 a 26 c 21 g 31 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 20.7 Length: 121
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-856-070-26 (1-c) x AX425084 (1-121)
 QY 1 GluAspTyrGluGlu 5
 |||||
 DB 56 CAACACTATGAGAA 70
 RESULT 3
 LOCUS GL4949 250 bp DNA linear SIS 30 MAR 2000
 DEFINITION SHGC 14798 Human homo sapiens STS genomic, sequence tagged site.
 ACCESSION GL4949
 VERSION GL4949.1 GI:1131712
 KEYWORDS STS.
 SOURCE Homo sapiens.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 250)
 AUTHORS Olivier, M. and Cox, D.P.
 TITLE Unpublished, Olivier, M., Cox, D.P. (2000)
 JOURNAL Unpublished (2000)
 COMMENT Contact: Michael Olivier, David R. Cox
 Stanford Human Genome Center
 Stanford University School of Medicine
 4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
 Tel: (650) 320-5800
 Fax: (650) 320-5801
 Email: olivier-shgc.stanford.edu
 Primer A: TGTGCACTATGAGTTTAATTG;
 Primer B: ACAAGATGAGTTTCTTCAGGTTG
 STS size: 139
 PCR Profile:
 Initial incubation: 94 degrees C for 90 seconds
 Denaturation: 94 degrees C for 15 seconds
 Annealing: 62 degrees C for 24 seconds
 Polymerization: 72 degrees C for 30 seconds
 PCR Cycles: 30
 Thermal Cycler: Perkin Elmer 9600
 PROTOCOL
 Template: 25 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Taq Polymerase: 0.05 units/ul
 total Vol: 10 ul
 Buffer: MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.3
 FEATURES
 source
 Location/Qualifiers
 1..250
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="3"
 /cloneLib="Human"
 STS
 primer_bind 6..144
 primer_bind 6..128
 BASE COUNT 91 a 35 c 39 g 83 t 2 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 47.2 Length: 250
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-856-070-26 (1-5) x G14449 (1-250)

QY 1 GlnAspTyrGluGlu 5
 Db 168 CAAGATTATGAGAG 182

RESULT 4

MMY14106/c
 LOCUS MMY14106 291 bp DNA linear W90 08 JAN 1994
 DEFINITION Mus musculus pkd2 exon 2.
 ACCESSION Y14106
 VERSION Y14106.1 GI:4107457
 KEYWORDS pkd2 gene; polycystin.
 SOURCE house mouse
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 291)
 AUTHORS Pennepkamp, P.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-1997) P. Pennepkamp, Westf. Wilhelms-Universitaet,
 Institut for Human Genetics, Vesaliusweg 12-14, D 48149 Muenster,
 FRG

REFERENCE 2 (bases 1 to 291)

AUTHORS Pennepkamp, P., Bogdanova, N., Wilda, M., Markoff, A., Hamelster, H.,
 Horst, J., and Dworniczak, P.
 TITLE Characterization of the murine polycystic kidney disease (pkd2)
 gene

JOURNAL Mamm. Genome 9 (9), 749-752 (1998)
 MEDLINE 98384541
 PUBMED 9716661

COMMENT Overlapping sequences: I.M.A.G.E. clones 45813 (Acc. No. EST:
 AA023786), and 316818 (Acc. No. EST: W11044)
 I.M.A.G.E. clones were obtained from the Resource Center/Primary
 Database of the German Human Genome Project, Max Planck Inst. for
 Molecular Genetics, Berlin.

FEATURES

source 1..291
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="1-J-15"
 /clone="201-L-2"
 /clone_lib="BAC genomic library, Research Genetics"
 gene 1..291
 /gene="pkd2"
 intron <1..72
 /number=1
 exon 73..186
 /gene="pkd2"
 /number=2
 intron 187..291
 /gene="pkd2"
 /number=2

BASE COUNT 62 a 73 c 80 g 76 t

ALIGNMENT

Alignment Scores:
 Pred. No.: 56.2 Length: 291
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-856-070-26 (1-5) x MMY14106 (1-291)

QY 1 GlnAspTyrGluGlu 5
 Db 179 CAAGACTACGAGAA 165

RESULT 5

AF411051
 LOCUS Emydoidea blandingii clone Bb1 15 microsatellite sequence.
 DEFINITION Emydoidea blandingii clone Bb1 15 microsatellite sequence.
 ACCESSION AF411051
 VERSION AF411051.1 GI:15705858
 KEYWORDS
 SOURCE
 ORGANISM Emydoidea blandingii.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Testudines; Cryptodira; Testudinoidae; Testudinidae; Emydoidea.
 REFERENCE 1 (bases 1 to 292)
 AUTHORS Osenkowski, M.F., Mockford, S., Wright, J.M., Snyder, M., Herman, T.B.,
 and Hughes, C.R.
 TITLE Isolation and characterization of microsatellite loci from the
 Blanding's turtle, Emydoidea blandingii
 JOURNAL Mol. Ecol. Notes 2 (2), 147-149 (2002)
 REFERENCE 2 (bases 1 to 292)
 AUTHORS Mockford, S.W., Wright, J.M., Snyder, M. and Herman, T.B.
 TITLE Direct Submission
 JOURNAL Submitted (16-AUG-2001) Biology, Dalhousie University, Halifax, NS
 B3H 4J1, Canada

FEATURES

source 1..292
 /organism="Emydoidea blandingii"
 /db_xref="taxon:85613"
 /clone="Bb1 15"
 repeat_region 1..292
 /note="microsatellite"
 /rpt_type=tandem
 BASE COUNT 97 a 46 c 60 g 89 t 10 others

Alignment Scores:
 Pred. No.: 56.4 Length: 292
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-09-856-070-26 (1-5) x AF411051 (1-292)

QY 1 GlnAspTyrGluGlu 5
 Db 11 CAGGACTACGAGAA 25

RESULT 6

G65316
 LOCUS SMCY-M55 Random genomic STS Homo sapiens STS genomic, sequence
 DEFINITION tagged site.
 ACCESSION G65316
 VERSION G65316.1 GI:9211152
 KEYWORDS STS.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 382)
 AUTHORS Oefner, P.J.
 TITLE Human random genomic STS survey, unpublished data
 JOURNAL Unpublished (1999)
 COMMENT

Contact: Peter Oefner
 Stanford Genome Center
 Stanford University
 855 California Ave., Palo Alto, CA 94304, USA
 Tel: 6508121926
 Fax: 6508121975
 Email: oefner@genome.stanford.edu
 Primer A: GGTAGGCTTTCAGAGTAG
 Primer B: GTTCTTGTGTAATGCTGAG

STS size: 382
 PCR Profile:
 Initial denaturing step of 95 degrees C for 10 min to activate
 AmpliTaq
 Gold (1 min for AmpliTaq):
 14 cycles of touchdown: 94 degrees C for 20 sec, annealing for 1
 min at 63
 degrees C to
 56 degrees C using decrements of 0.5 degrees C, extension at 72
 degrees C
 for 1 min;
 20 cycles at 94 degrees C for 20s, 56 degrees C for 45 sec, 72
 degrees C
 for 1 min.
 Protocol:
 Template: 50 ng
 Primer: each 0.2 uM
 Taq polymerase: 0.02 units/ul
 Total Vol: 50 ul

Buffer: MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 8.3
 DMSO: 0 %
 Location/Qualifiers
 1..382

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo;
 Stenasson, H., Steinhorsdottir, V. and Gulcher, J. R.
 Human schizophrenia gene
 Patent: WO 0164876-A 1174 07-SEP-2001;
 Decode Genetics PHF. (US)

FEATURES
 primer_bind
 1..19
 primer_bind
 complement(363..382) 84 t
 BASE COUNT 147 a 70 c 81 g 84 t
 ORIGIN

Alignment Scores:
 Pred. No.: 76.5 Length: 382
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-856-070-26 (1-5) x G65316 (1-382)

QY 1 GlnAspTyrGluGlu 5
 |||||

DB 365 CAAGATTATGAGAA 479

RESULT 7

AX270543/c
 LOCUS
 AX270543
 DEFINITION
 Sequence 1174 from Patent WO0164876.
 ACCESSION
 AX270543.1 GI:16543119
 VERSION
 AX270543.1 GI:16543119
 KEYWORDS
 human.
 SOURCE
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 AUTHORS
 Stenasson, H., Steinhorsdottir, V. and Gulcher, J. R.
 Human schizophrenia gene
 Patent: WO 0164876-A 1174 07-SEP-2001;
 Decode Genetics PHF. (US)
 TITLE
 Human schizophrenia gene
 JOURNAL
 Submitted (05-MAR-1998) Hunter S.J., Veterinary Parasitology,
 Glasgow University, Bearsden Road, Glasgow, G61 1QH, UK
 2 (bases 1 to 436)
 Stage specific gene expression in the post-infective L3 of the
 filarial nematode, Brugia pahangi

FEATURES
 source

1..401
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 112 a 75 c 104 g 109 t 1 others

ORIGIN

Alignment Scores:
 Pred. No.: 80.9 Length: 401
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-856-070-26 (1-5) x AX270543 (1-401)

QY 1 GlnAspTyrGluGlu 5
 |||||

DB 379 CAAGATTATGAGAA 365

RESULT 8

AX272074/c
 LOCUS
 AX272074
 DEFINITION
 Sequence 1174 from Patent WO0164877.
 ACCESSION
 AX272074
 VERSION
 AX272074.1 GI:16544811
 KEYWORDS
 human.
 SOURCE
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 AUTHORS
 Stenasson, H., Steinhorsdottir, V. and Gulcher, J. R.
 Human schizophrenia gene
 Patent: WO 0164877-A 1174 07-SEP-2001;
 Decode Genetics PHF. (US)
 TITLE
 Human schizophrenia gene
 JOURNAL
 Submitted (05-MAR-1998) Hunter S.J., Veterinary Parasitology,
 Glasgow University, Bearsden Road, Glasgow, G61 1QH, UK
 2 (bases 1 to 436)
 Stage specific gene expression in the post-infective L3 of the
 filarial nematode, Brugia pahangi

FEATURES
 source

1..401
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 112 a 75 c 104 g 109 t 1 others

Alignment Scores:

Pred. No.: 80.9 Length: 401
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-856-070-26 (1-5) x AX272074 (1-401)

QY 1 GlnAspTyrGluGlu 5
 |||||

DB 379 CAAGATTATGAGAA 365

RESULT 9

HPA224967
 LOCUS
 HPA224967
 DEFINITION
 Brugia pahangi mRNA for troponin (isolate sj5).
 ACCESSION
 A7224967
 VERSION
 A7224967.1 GI:2959347
 KEYWORDS
 troponin.
 SOURCE
 Brugia pahangi.
 ORGANISM
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 Onchocercidae; Brugia.
 1 (bases 1 to 436)
 Hunter, S.J.
 Direct Submission
 Submitted (05-MAR-1998) Hunter S.J., Veterinary Parasitology,
 Glasgow University, Bearsden Road, Glasgow, G61 1QH, UK
 2 (bases 1 to 436)
 Stage specific gene expression in the post-infective L3 of the
 filarial nematode, Brugia pahangi

REFERENCE

AUTHORS
 Hunter, S.J.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (05-MAR-1998) Hunter S.J., Veterinary Parasitology,
 Glasgow University, Bearsden Road, Glasgow, G61 1QH, UK
 2 (bases 1 to 436)
 Stage specific gene expression in the post-infective L3 of the
 filarial nematode, Brugia pahangi

FEATURES
 source

112 a 75 c 104 g 109 t 1 others

JOURNAL Mol. Biochem. Parasitol. 79 (1), 109-112 (1996)

MEDLINE 97001646

PUBMED 8844678

FEATURES

source

Location/Qualifiers

1..436 /organism="Brugia pahangi"

/isolate="sjs"

/db_xref="taxon:6280"

/dev_stage="3 days p 1.L3: vector derived L3"

62..>436

/codon_start=1

/product="tropenin"

/protein_id="CAA12260.1"

/db_xref="GI:2959348"

/db_xref="SPTPMR1:045212"

/translation="MADEEELTEDEEVEEVEEAAAEAPAPASADDEAPAE"

AEATPRLRAPPEKDETPAEUTAPKAMLAARKKHDEEAAKIQDVHFRPKIEKEI

EEELRTLKEKQRPQRPQRPK"

BASE COUNT 188 a 73 c 109 g 66 t

ORIGIN

Alignment Scores:

Pred. No.: 89 Length: 436

Score: 28.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 3 Gaps: 0

US-09-856-070-26 (1-5) x RPA224957 (1-436)

QY 1 GlnAspTyrGluGlu 5

DB 326 CAGATTACGAGAA 140

RESULT 10

SPU31922/c

LOCUS 437 bp DNA linear BCT 21 NOV-1999

DEFINITION Streptococcus pyogenes GTP-binding protein gene homolog, partial

cds.

ACCESSION U31922

VERSION 031922.1

KEYWORDS 21.6456499

SOURCE Streptococcus pyogenes.

ORGANISM Streptococcus pyogenes.

REFERENCE 1 (bases 1 to 437)

AUTHORS Wolosinski, M. and Podbielski, A.

TITLE Direct Submission

JOURNAL Submitted (18-MAY-1995) Markus Wolosinski, RWTH Aachen, Institute of

Medical Microbiology, Pauwelsstrasse 40, Aachen, NRW 52074, Germany

Location/Qualifiers

1..437 /organism="Streptococcus pyogenes"

/strain="CS101"

/db_xref="taxon:1314"

<1..>437

/note="similar to the spo0B product of B. subtilis.

Swiss-Prot Accession Number P20964"

/codon_start=2

/transl_table=11

/product="GTP-binding protein homolog"

/protein_id="AAF09165.1"

/db_xref="GI:645630"

/translation="WPTVVDAPTKVITDI VHQGPVVI AKGRPGGCHNIRFATPRN

PAPEIAENGQERQIELEKILADVGIVGPPSGVKSTLLSVVSSAKPKIGAYHFTT

IVNIGMVFVKSDSPFAMADLPGLLEGASQGVIGTQFLRHPPA"

BASE COUNT 109 a 84 c 119 g 125 t

ORIGIN

Alignment Scores:

Pred. No.: 89 2 Length: 437

Score: 28.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

US-09-856-070-26 (1-5) x SPU31922 (1-437)

QY 1 GlnAspTyrGluGlu 5

DB 137 CAGATTACGAGGAG 123

RESULT 11

LOCUS 441 bp DNA linear FAT 14 JUN 2002

DEFINITION Sequence 3233 from Patent WO0259103.

ACCESSION AX410586

VERSION AX410586.1

KEYWORDS GI:21444291

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Alvares, C., Horne, B., Barros da Silva, S. and Voelkel, J. G.

TITLE Gene expression profiles in liver cancer

JOURNAL Patent: WO 0259103-A 3233 11 APR 2002;

GENE LOGIC INC (US)

FEATURES Location/Qualifiers

SOURCE 1..441

/organism="Homo sapiens"

/db_xref="taxon:9606"

/note="EMBL/GenBank Accession No. T83397"

BASE COUNT 115 a 92 c 124 g 103 t

ORIGIN 7 others

Alignment Scores:

Pred. No.: 90.1 Length: 441

Score: 28.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-856-070-26 (1-5) x AX410586 (1-441)

QY 1 GlnAspTyrGluGlu 5

DB 98 CAGCATTACCGGAA 112

RESULT 12

AB024579/c

LOCUS 448 bp DNA linear FPI 04 APR 2002

DEFINITION Homo sapiens Hsp1 gene for translocation protein 1, exon 3.

ACCESSION AB024581

VERSION AB024581.1

KEYWORDS GI:9971198

SEGMENT translocation protein 1; HTP1.

SOURCE 3 of 8

ORGANISM Homo sapiens DNA.

REFERENCE 1

AUTHORS Fukuyama, T.

TITLE Fine structure of the human translocation protein 1 (HTP1/TL0C1)

JOURNAL Daimon, M., Susa, S. and Kato, T.

MEDLINE 109MB Life 48 (6), 619-624 (1999)

REFERENCE 2 (bases 1 to 448)

AUTHORS Daimon, M.

TITLE Direct Submission

JOURNAL Submitted (05 MAR 1999) Makoto Daimon, Yamagata University School

of Medicine, the third department of Internal Medicine, 2-2-2

Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-856-070-26 {1-5} x AX154*65 (1-520)

QY 1 GlnAsplyrGluGlu 5

|||||

Db 204 CAGGACTACGAGGAA 218

Search completed: January 16, 2003, 19:06:09
 Job time : 443.214 secs

